



FIGURE S2.—Q-RT-PCR confirmation of microarray data. Ten genes were selected from the microarray dataset and confirmed independently via Q-RT-PCR; all ten of these genes were significantly up-regulated in a wild-type cross compared to a cross homozygous for an NCU09915 deletion, and the Q-RT-PCR data confirms this result. In addition, the Q-RT-PCR data confirms that although the female of the homozygous deletion cross was present as a heterokaryon with the helper strain, no NCU09915 (*fsd-1*) RNA is present in the perithecial tissue of this cross.